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Fig.1.

```

      10      20      30      40
      *      *      *      *
ATG GAG CGC TGC CCC AGC CTA GGG GTC ACC CTC TAC GCC CTG GTG
M E R C P S L G V T L Y A L V>

      50      60      70      80      90
      *      *      *      *      *
GTG GTC CTG GGG CTG CCG GCG ACA CCG GCC GGC GGC CAG CAC TAT
V V L G L R A T P A G G Q H Y>

      100     110     120     130
      *      *      *      *
CTC CAC ATC CGC CCG GCA CCC AGC GAC AAC CTG CCC CTG GTG GAC
L H I R P A P S D N L P L V D>

      140     150     160     170     180
      *      *      *      *      *
CTC ATC GAA CAC CCA GAC CCT ATC TTT GAC CCC AAG GAA AAG GAT
L I E H P D P I F D P K E K D>

      190     200     210     220
      *      *      *      *
CTG AAC GAG ACG CTG CTG CCG TCG CTG CTC GGG GGC CAC TAC GAC
L N E T L L R S L L G G H Y D>

      230     240     250     260     270
      *      *      *      *      *
CCA GGC TTC ATG GCC ACC TCG CCC CCC GAG GAC CCG CCC GGC GGC
P G F M A T S P P E D R P G G>

      280     290     300     310
      *      *      *      *
GGC GGG GGT GCA GGT GGG GGC GCG GAG GAC CTG GCG GAG CTG GAC
G G G A A G G A E D L A E L D>

      320     330     340     350     360
      *      *      *      *      *
CAG CTG CTG CCG CAG CCG CCG TCG GGG GCC ATG CCG AGC GAG ATC
Q L L R Q R P S G A M P S E I>

      370     380     390     400
      *      *      *      *
AAA GGG CTA GAG TTC TCC GAG GGC TTG GCC CAG GGC AAG AAG CAG
K G L E F S E G L A Q G K K Q>

      410     420     430     440     450
      *      *      *      *      *
CGC CTA AGC AAG AAG CTG CCG AGG AAG TTA CAG ATG TGG CTG TGG
R L S K K L R R R L Q M W L W>

      460     470     480     490
      *      *      *      *
TCG CAG ACA TTC TGC CCC GTG CTG TAC GCG TGG AAC GAC CTG GGC
S Q T F C P V L Y A W N D L G>

      500     510     520     530     540
      *      *      *      *      *
AGC CGC TTT TGG CCG CCG TAC GTG AAG GTG GGC AGC TGC TTC AGT
S R F W P R Y V K V G S C F S>

```

Fig.1. (cont.)

			550				560				570				580	—
			*				*				*				*	
AAG	CGC	TCG	TGC	TCC	GTG	CCC	GAG	GGC	ATG	GTG	TGC	AAG	CCG	TCC		
K	R	S	C	S	V	*P	E	G	M	V	C	K	P	S>		
			590				600				610				620	
			*				*				*				*	
AAG	TCC	GTG	CAC	CTC	ACG	GTG	CTG	CGG	TGG	CGC	TGT	CAG	CGG	CGC		
K	S	V	H	L	T	V	L	R	W	R	C	Q	R	R>		
			640				650				660				670	
			*				*				*				*	
GGG	GGC	CAG	CGC	TGC	GGC	TGG	ATT	CCC	ATC	CAG	TAC	CCC	ATC	ATT		
G	G	Q	R	C	G	W	I	P	I	Q	Y	P	I	I>		
			680				690									
			*				*									
TCC	GAG	TGC	AAG	TGC	TGC	TGC	TGC	TGC	TGC	TGC	TGC	TGC	TGC	TGC	TGC	TGC
S	E	C	K	C	S	C	*>									

00007333 070001  
T0000000

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Fig. 2A.

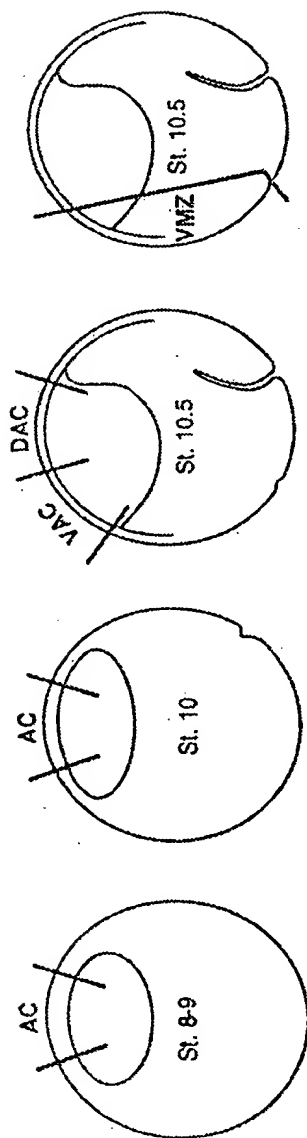


Fig. 2B.

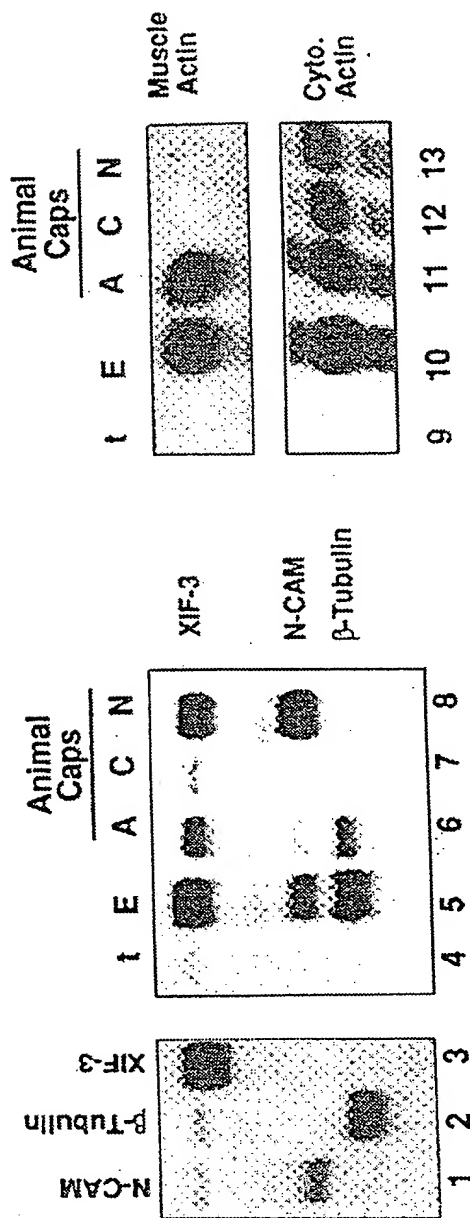


Fig. 3.

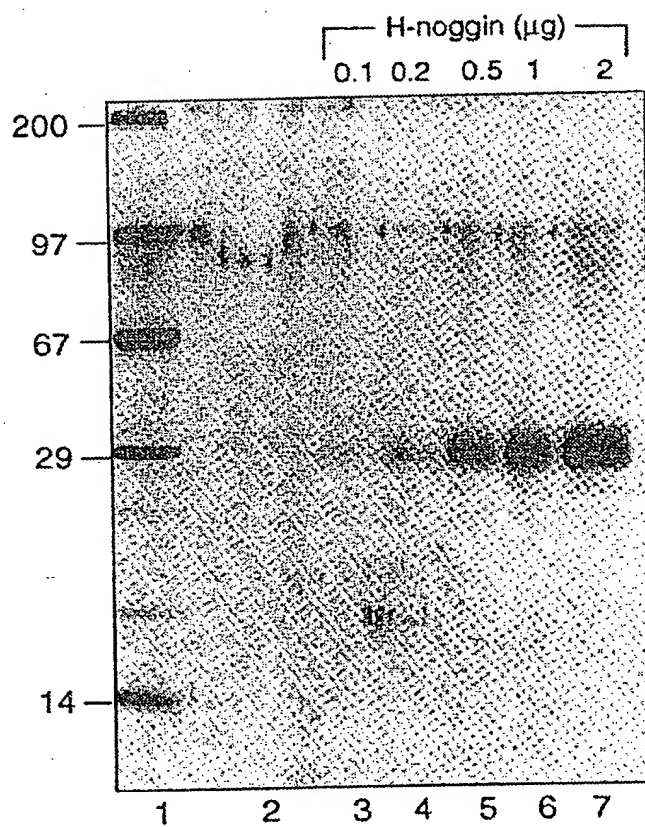
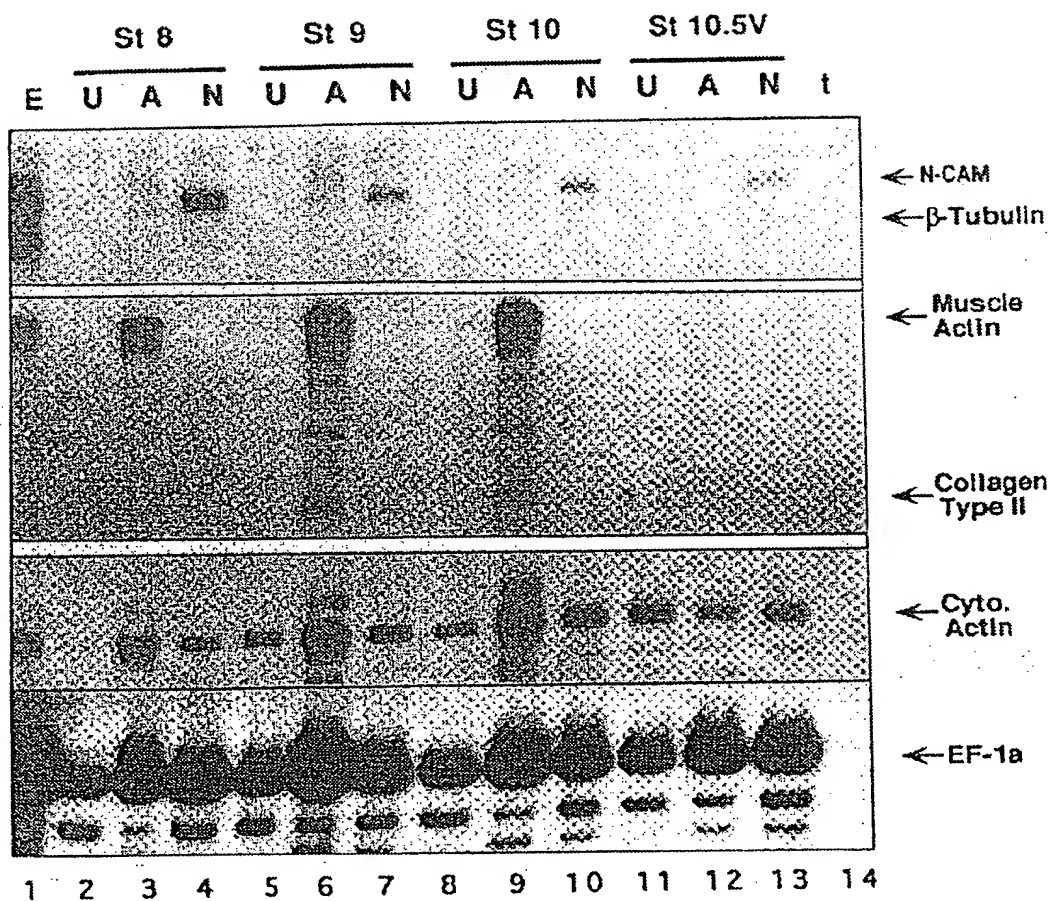
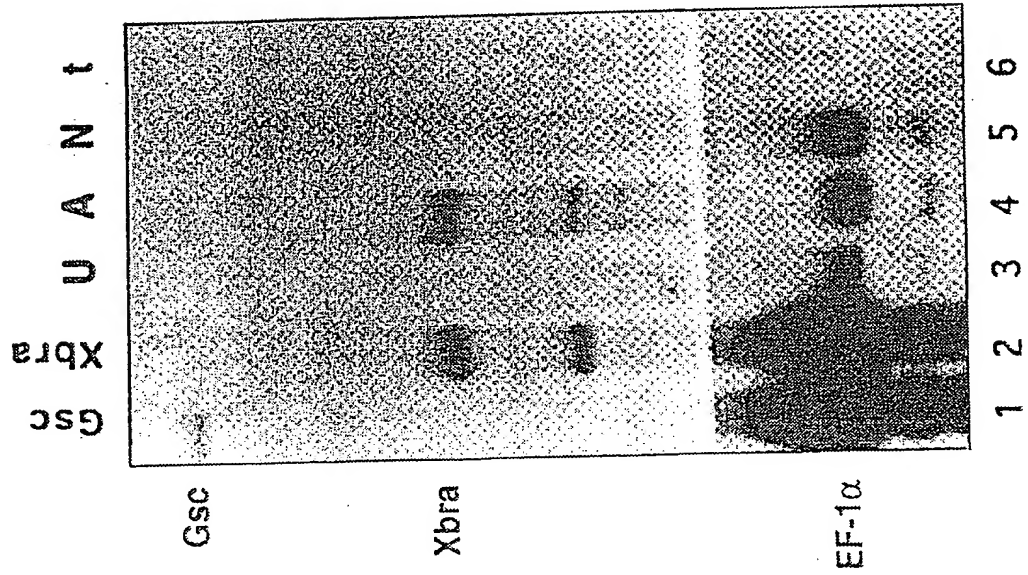


Fig. 4A.



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Fig. 4B.



6/15

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Fig. 4C.

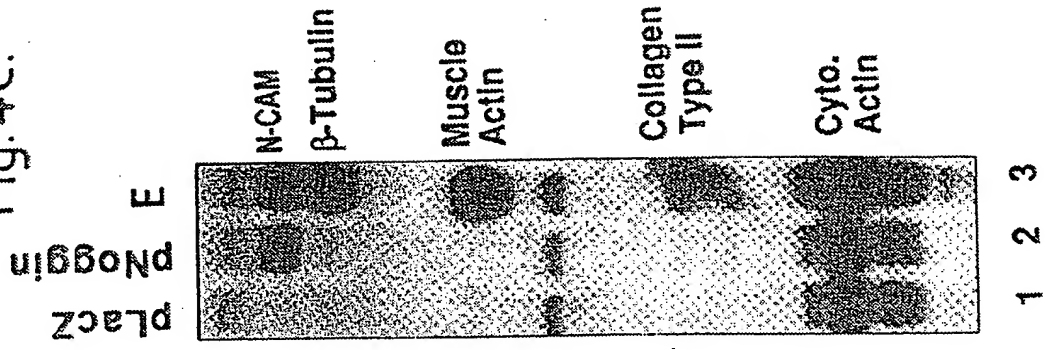
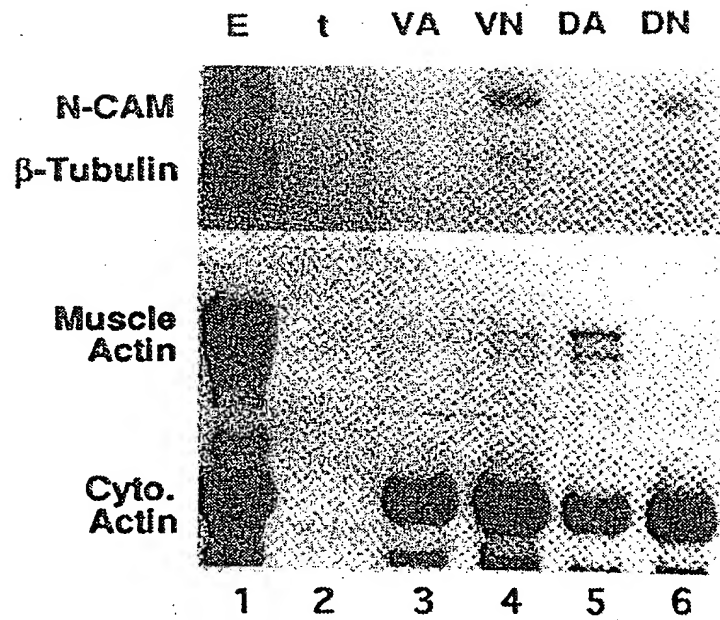


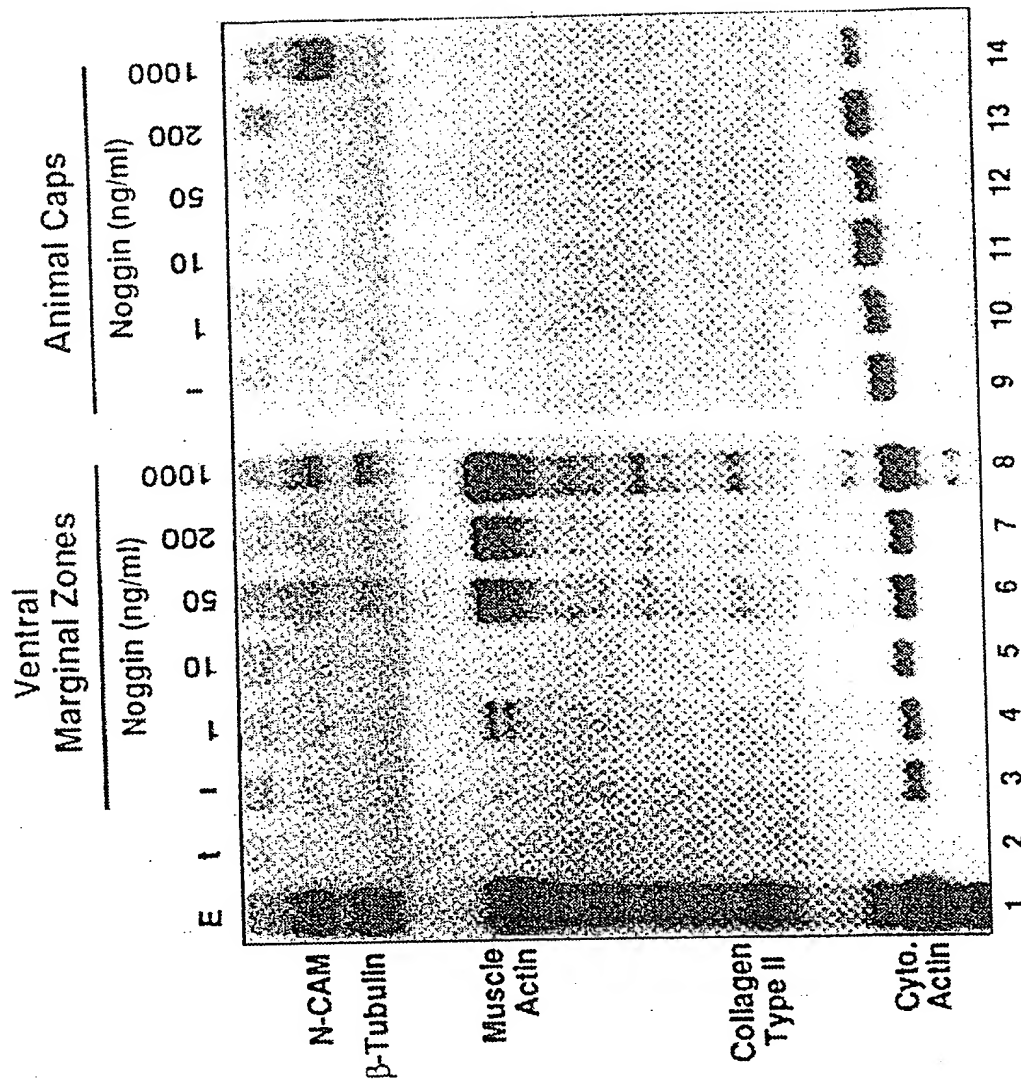
Fig.5.





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Fig.6.



102020" 22E46860

Fig. 7A.

N-CAM

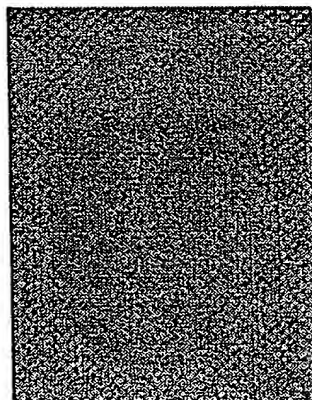


Fig. 7B.

N-CAM

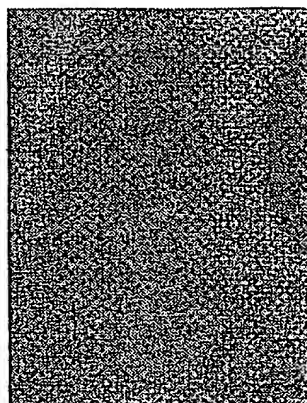


Fig. 7C.

Muscle Actin

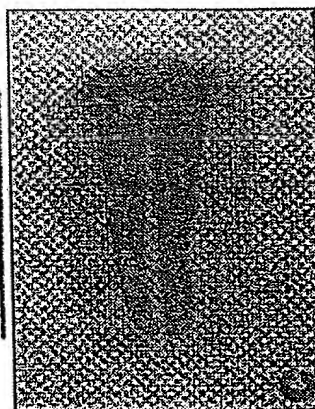
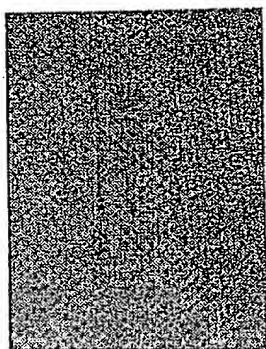


FIG. 7D. Embryo

Fig.7D.  
Embryo



GF11

Fig.7E.  
+ Noggin

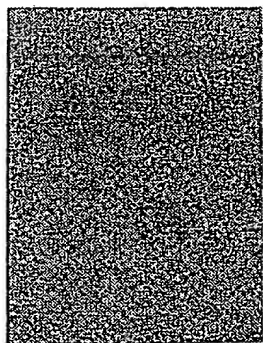
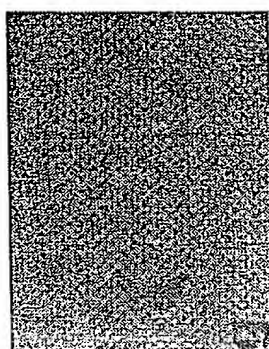


Fig.7G



XAG

Fig.7H.

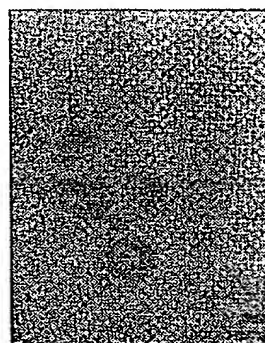
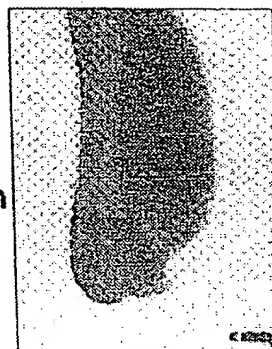


Fig.7J.



OTX

Fig.7F.  
Untreated

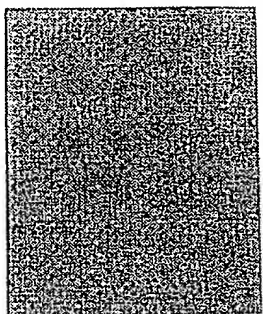


Fig.7I.

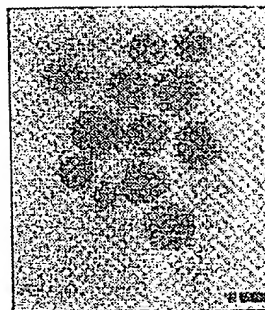
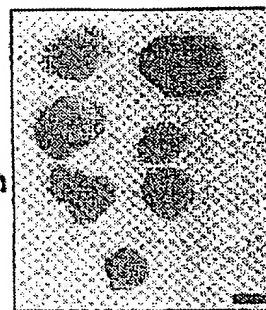


Fig.7L.



89

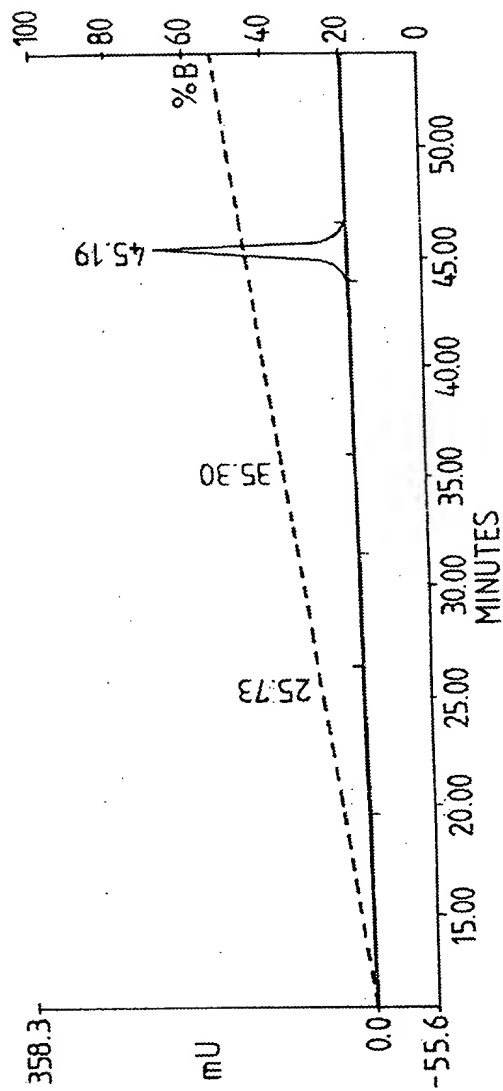
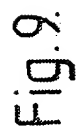


Fig.10

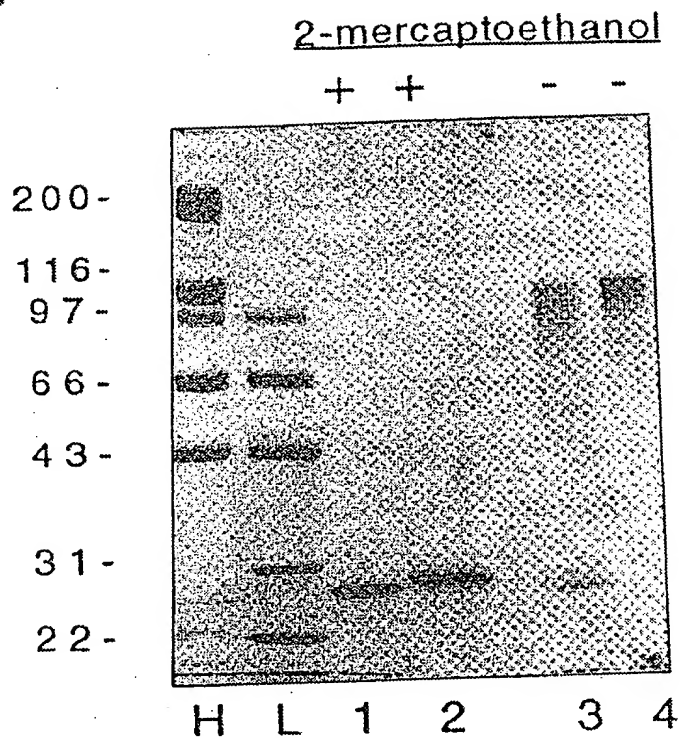


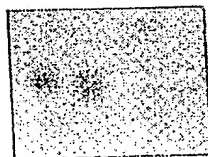
Fig.12.

Bacterial

H-nog

(μg/ml)

10 2 0.5 0.1

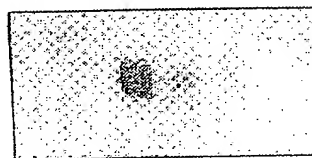


Baculovirus

Mock H-nog

(μg/ml)

1 0.2 1 0.2 0.05 0.01

muscle  
actin

12/15

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Fig. 11.

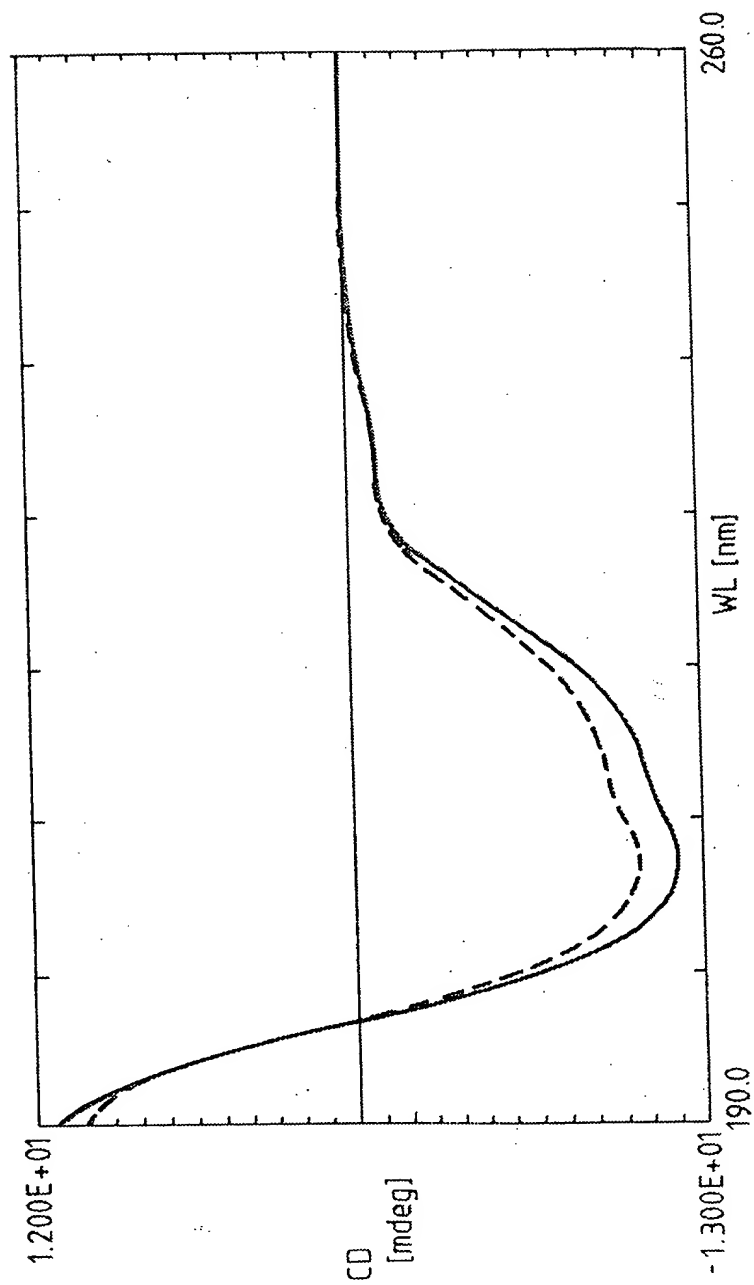


Fig.13.

5 10 15 20 25 30 35 40 45 50 55 60  
 TAACTCACTC ATTAGNCACC CCAGCCTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG  
 65 70 75 80 85 90 95 100 105 110 115 120  
 GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA TGACCATGAT TACGCCAAGC  
 125 130 135 140 145 150 155 160 165 170 175 180  
 TCGAAATTAA CCCTCACTAA AGGGAACAAA AGCTGGAGCT CCACCGCGGT GGCGGCCGCC  
 185 190 195 200 205 210 215 220 225 230 235 240  
 TTCCCAAGTA GAGCGGCGGG GGGGAATTGC GACCAACTCG TGCGGTCTT CTGCNCCGGC  
 245 250 255 260 265 270 275 280 285 290 295 300  
 GCGGGAGCCG GCGCTGCGCG ACCGGCTCTC CTCGCAGCTC ATGCTGCCTG CCCTGCGCCT  
 305 310 315 320 325 330 335 340 345 350 355 360  
 GCTCAGCCTC GGGTGAGCCA CCTCCGGAGG GACCGGGGAG CGCGGCAGCG CCGCGGACTC  
 365 370 375 380 385 390 395 400 405 410 415 420  
 GGCSTGCTCT CCTCCGGGGA CGCGGGACGA AGAGGCAGCC CCGGGGCGCG CGCGGGAGGC  
 425 430 435 440 445 450 455 460 465 470 475 480  
 ATGGAGCGCT GCCCAGCCT GGGGGTCACC CTCTACGCCC TGGTGGTGGT CCTGGGGCTG  
 M E R C P S L G V T L Y A L V V V L G L>  
 485 490 495 500 505 510 515 520 525 530 535 540  
 CGGGCAGCAC CAGCCGGCGG CCAGCACTAT CTACACATCC GCCCAGCACC CAGCGACAAC  
 R A A P A G G Q H Y L H I R P A P S D N>  
 545 550 555 560 565 570 575 580 585 590 595 600  
 CTGCCCTTGG TGGACCTCAT CGAACATCCA GACCCTATCT TTGACCCTAA GGAGAAGGAT  
 L P L V D L I E H P D P I F D P K E K D>  
 605 610 615 620 625 630 635 640 645 650 655 660  
 CTGAACGAGA CGCTGCTGCG CTCGCTGCTC GGGGGCCACT ACGACCCGGG CTTTATGGCC  
 L N E T L L R S L L G G H Y D P G F M A>  
 665 670 675 680 685 690 695 700 705 710 715 720  
 ACTTCGCCCC CAGAGGACCG ACCCGGAGGG GGCGGGGGAC CGGCTGGAGG TGCCGAGGAC  
 T S P P E D R P G G G G G P A G G A E D>  
 725 730 735 740 745 750 755 760 765 770 775 780  
 CTGGCGGAGC TGGACCAGCT GCTGCGGCAG CGGCCGTCGG GGGCCATGCC GAGCGAGATC  
 L A E L D Q L L R Q R P S G A M P S E I>  
 785 790 795 800 805 810 815 820 825 830 835 840  
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15/15

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